



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 077319/0125

*In re patent application of*

David W. LEUNG *et al.*

Serial No. 08/842,827

Group Art Unit: 1801

Filed: April 17, 1997

Examiner: Unassigned

For: HUMAN PHOSPHATIDIC ACID PHOSPHATASE

STATEMENT TO SUPPORT FILING AND SUBMISSION IN ACCORDANCE  
WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents  
Washington, D.C. 20231  
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

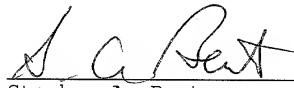
1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter; and

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

5 August 1997

Date

  
Stephen A. Bent  
Reg. No. 29,768

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: LEUNG, David W.  
TOMPKINS, Christopher K.

(ii) TITLE OF INVENTION: HUMAN PHOSPHATIDIC ACID PHOSPHATASE

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Foley & Lardner  
(B) STREET: 3000 K Street, N.W., Suite 500  
(C) CITY: Washington  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20007-5109

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/842,827  
(B) FILING DATE: 17-APR-1997  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: BENT, Stephen A.  
(B) REGISTRATION NUMBER: 29,768  
(C) REFERENCE/DOCKET NUMBER: 77319/125

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (202) 672-5300  
(B) TELEFAX: (202) 672-5399  
(C) TELEX: 904136

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1563 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 342..1193

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 342..1193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT  
GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACCA CGAGCGCCTC GGCACTAACC

60

120

GAGTGTTCGC GGGGCTGTG AGGGGAGGGC CCCGGGCC ATTGCTGGC GTGGGAGCGC	180
CGCCCGGTCT CAGCCCGGCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG CCGCTATCTC	240
GGGGCCGTCG CCAGCCCGGG CCCGGGCTCG ATAATCAAGG GCCTCGGCC TCGTCCCGCA	300
CCTCATTCCA TCGCCCTTGC CGGGCAGCCC GGGCAGAGAC C ATG TTT GAC AAG Met Phe Asp Lys 1	353
ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala 5 10 15 20	401
GGA TTG CCT TTT GCA ATT CTT ACT TCA AGG CAT ACC CCC TTC CAA CGA Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg 25 30 35	449
GGA GTA TTC TGT AAT GAT GAG TCC ATC AAG TAC CCT TAC AAA GAA GAC Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro Tyr Lys Glu Asp 40 45 50	497
ACC ATA CCT TAT GCG TTA TTA GGT GGA ATA ATC ATT CCA TTC AGT ATT Thr Ile Pro Tyr Ala Leu Leu Gly Ile Ile Ile Pro Phe Ser Ile 55 60 65	545
ATC GTT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC TGT AAC CTT TTG Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn Leu Leu 70 75 80	593
CAC TCA AAT TCC TTT ATC AGG AAT AAC TAC ATA GCC ACT ATT TAC AAA His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile Tyr Lys 85 90 95 100	641
GCC ATT GGA ACC TTT TTA TTT GGT GCA GCT GCT AGT CAG TCC CTG ACT Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser Gln Ser Leu Thr 105 110 115	689
GAC ATT GCC AAG TAT TCA ATA GGC AGA CTG CGG CCT CAC TTC TTG GAT Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe Leu Asp 120 125 130	737
GTT TGT GAT CCA GAT TGG TCA AAA ATC AAC TGC AGC GAT GGT TAC ATT Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr Ile 135 140 145	785
GAA TAC TAC ATA TGT CGA GGG AAT GCA GAA AGA GTT AAG GAA GGC AGG Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu Gly Arg 150 155 160	833
TTC TTC TAT TCA GGC CAC TCT TCG TTT TCC ATG TAC TGC ATG CTG Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu 165 170 175 180	881
TTT GTG GCA CTT TAT CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA AGA Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg 185 190 195	929
CTC TTA CGC CCC ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC ATT TAT Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser Ile Tyr 200 205 210	977
GTG GGC CTT TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG AGC GAT GTG Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val 215 220 225	1025

TTG ACT GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA TTA GTT GCT GTA Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala Val 230 235 240	1073
TAT GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT TTT AAA GAA AGA AAA Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg Lys 245 250 255 260	1121
GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT GGG AAT Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr Gly Asn 265 270 275	1169
CAC TAT CCG AGC AAT CAC CAG CCT TGAAAGGCAG CAGGGTGCCTC AGGTGAAGCT His Tyr Pro Ser Asn His Gln Pro 280	1223
GGCCTGTTTCTAAAGAAAATGATTGCCA CAAGGCAAGA GGATGCATCT TTCTTCCTGG TGTACAAGCC TTTAAAGACT TCTGCTGCTG ATATGCCTCT TGGATGCACA CTTTGTGTGT ACATAGTTAC CTTAACTCA GTGGTTATCT AATAAGCTCA AACTCATTAA AAAAAGTCCA AGCCTTCCAC CAAAACAGTG CCCCACCTGT ATACATTTTT ATTAAAAAAA TGTAATGCTT ATGTATAAAC ATGTATGTAATATGCTTCT ATGAATGATG TTTGATTTAA ATATAATACA TATTAAAATG TATGGGAGAA CCAAAAAAAA AAAAAAAA	1283 1343 1403 1463 1523 1563

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 284 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys 1 5 10 15
Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr 20 25 30
Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro 35 40 45
Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile 50 55 60
Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr 65 70 75 80
Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala 85 90 95
Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser 100 105 110
Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro 115 120 125
His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser 130 135 140

Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val  
145 150 155 160

Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met  
165 170 175

Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly  
180 185 190

Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala  
195 200 205

Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His  
210 215 220

Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile  
225 230 235 240

Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe  
245 250 255

Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro  
260 265 270

Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
275 280

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 342..1196

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 342..1196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTGTTGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT 60  
GAGGAGGTCC TGAGGCTACA GAGCTGCCG GCCTGGCACA CGAGCGCCTC GGCACTAACC 120  
GAGTGTTCGC GGGGCTGTG AGGGGAGGGC CCCGGCGCC ATTGCTGGCG GTGGGAGCGC 180  
CGCCCGGTCT CAGCCCGCCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC 240  
GGGGCCGTCTG CCAGCCCCGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCCCGCA 300  
CCTCATTCCA TCGCCCTTGC CGGGCAGGCC GGGCAGAGAC C ATG TTT GAC AAG 353  
Met Phe Asp Lys  
1

ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT  
Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala  
5 10 15 20 401

TCC ATG CCT ATG GCT GTT CTA AAA TTG GGC CAA ATA TAT CCA TTT CAG Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile Tyr Pro Phe Gln 25 30 35	449
AGA GGC TTT TTC TGT AAA GAC AAC AGC ATC AAC TAT CCG TAC CAT GAC Arg Gly Phe Cys Lys Asp Asn Ser Ile Asn Tyr Pro Tyr His Asp 40 45 50	497
AGT ACC GCC GCA TCC ACT GTC CTC ATC CTA GTG GGG GTT GGC TTG CCC Ser Thr Ala Ala Ser Thr Val Leu Ile Leu Val Gly Val Gly Leu Pro 55 60 65	545
GTT TCC TCT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC TGT AAC CTT Val Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn Leu 70 75 80	593
TTG CAC TCA AAT TCC TTT ATC AGT AAT AAC TAC ATA GCC ACT ATT TAC Leu His Ser Asn Ser Phe Ile Ser Asn Asn Tyr Ile Ala Thr Ile Tyr 85 90 95 100	641
AAA GCC ATT GGA ACC TTT TTA TTT GGT GCA GCT GCT AGT CAG TCC CTG Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser Gln Ser Leu 105 110 115	689
ACT GAC ATT GCC AAG TAT TCA ATA GGC AGA CTG CGG CCT CAC TTC TTG Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe Leu 120 125 130	737
GAT GTT TGT GAT CCA GAT TGG TCA AAA ATC AAC TGC AGC GAT GGT TAC Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr 135 140 145	785
ATT GAA TAC TAC ATA TGT CGA GGG AAT GCA GAA AGA GTT AAG GAA GGC Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu Gly 150 155 160	833
AGG TTG TCC TTC TAT TCA GGC CAC TCT TCG TTT TCC ATG TAC TGC ATG Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met 165 170 175 180	881
CTG TTT GTG GCA CTT TAT CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala 185 190 195	929
AGA CTC TTA CGC CCC ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC ATT Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser Ile 200 205 210	977
TAT GTG GGC CTT TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG AGC GAT Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp 215 220 225	1025
GTG TTG ACT GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA TTA GTT GCT Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala 230 235 240	1073
GTA TAT GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT TTT AAA GAA AGA Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg 245 250 255 260	1121
AAA GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT GGG Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr Gly 265 270 275	1169
AAT CAC TAT CCG AGC AAT CAC CAG CCT TGAAAGGCAG CAGGGTGC Asn His Tyr Pro Ser Asn His Gln Pro 280 285	1216

AGGTGAAGCT	GGCCTGTTT	CTAAAGAAA	ATGATTGCCA	CAAGGCAAGA	GGATGCATCT	1276
TTCTTCCTGG	TGTACAAGCC	TTTAAAGACT	TCTGCTGCTG	ATATGCCTCT	TGGATGCACA	1336
CTTTGTGTGT	ACATAGTTAC	CTTTAACTCA	GTGGTTATCT	AATAGCTCTA	AACTCATTAA	1396
AAAAACTCCA	AGCCTTCCAC	CAAAACAGTG	CCCCACCTGT	ATACATTTTT	ATTAAAAAAA	1456
TGTAATGCTT	ATGTATAAAC	ATGTATGTAA	TATGCTTCT	ATGAATGATG	TTTGATTTAA	1516
ATATAATACA	TATTTAAATG	TATGGGAGAA	CCAAAAAAA	AAAAAAA	AAAAAAA	1566

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 285 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Phe	Asp	Lys	Thr	Arg	Leu	Pro	Tyr	Val	Ala	Leu	Asp	Val	Leu	Cys	
1						5				10					15	
Val	Leu	Leu	Ala	Ser	Met	Pro	Met	Ala	Val	Leu	Lys	Leu	Gly	Gln	Ile	
							20		25				30			
Tyr	Pro	Phe	Gln	Arg	Gly	Phe	Phe	Cys	Lys	Asp	Asn	Ser	Ile	Asn	Tyr	
	35						40					45				
Pro	Tyr	His	Asp	Ser	Thr	Ala	Ala	Ser	Thr	Val	Leu	Ile	Leu	Val	Gly	
	50					55				60						
Val	Gly	Leu	Pro	Val	Ser	Ser	Ile	Ile	Leu	Gly	Glu	Thr	Leu	Ser	Val	
	65						70			75			80			
Tyr	Cys	Asn	Leu	Leu	His	Ser	Asn	Ser	Phe	Ile	Ser	Asn	Asn	Tyr	Ile	
	85							90				95				
Ala	Thr	Ile	Tyr	Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ala	
	100						105					110				
Ser	Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg	
	115						120				125					
Pro	His	Phe	Leu	Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys	
	130					135				140						
Ser	Asp	Gly	Tyr	Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu	Arg	
	145					150				155			160			
Val	Lys	Glu	Gly	Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser	
					165				170				175			
Met	Tyr	Cys	Met	Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys	
						180			185			190				
Gly	Asp	Trp	Ala	Arg	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	Leu	Val	
						195			200			205				
Ala	Val	Ser	Ile	Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His	
						210				215			220			

His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala  
225 230 235 240

Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser  
245 250 255

Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr  
260 265 270

Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
275 280 285

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 294..1226

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 294..1226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCGCAGCTC TGCAAAAGTT TCTGCTCGGG ATCTGGCTCT CTTCGGCTTG GACTTTAGAA 60  
CGATTAGGG TTGACAGAGG AAAGCAGAGG CGCGCAGGGAG GAGCAGAAAA CACCACCTTC 120  
TGCAGTTGGA GGCAGGCAGC CCCGGCTGCA CTCTAGCCGC CGCGCCCGGA GCCGGGGCCG 180  
ACCCGGCCACT ATCCCGCAGCA GCCTCGGCCA GGAGGCGACC CGGGCGCCTG GGTGTGTGGC 240  
TGCTGTTGCG GGACGTCTTC GCGGGGGCGGG AGGCTCGCAGC CGCAGCCAGC GCC ATG  
Met 1

CAA AAC TAC AAG TAC GAC AAA GCG ATC GTC CCG GAG AGC AAG AAC GGC 344  
Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn Gly  
5 10 15

GCG AGC CCG GCG CTC AAC AAC AAC CCG AGG AGG AGC GGC AGC AAG CGG 392  
Gly Ser Pro Ala Leu Asn Asn Pro Arg Arg Ser Gly Ser Lys Arg  
20 25 30

GTG CTG CTC ATC TGC CTC GAC CTC TTC TGC CTC TTC ATG GCG GGC CTC 440  
Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly Leu  
35 40 45

CCC TTC CTC ATC ATC GAG ACA AGC ACC ATC AAG CCT TAC CAC CGA GGG 488  
Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg Gly  
50 55 60 65

TTT TAC TGC AAT GAT GAG AGC ATC AAG TAC CCA CTG AAA ACT GGT GAG 536  
Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly Glu  
70 75 80

ACA ATA AAT GAC GCT GTG CTC TGT GCC GTG GGG ATC GTC ATT GCC ATC Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala Ile 85 90 95	584
CTC GCG ATC ATC ACG GGG GAA TTC TAC CGG ATC TAT TAC CTG AAG AAG Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys Lys 100 105 110	632
TCG CGG TCG ACG ATT CAG AAC CCC TAC GTG GCA GCA CTC TAT AAG CAA Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys Gln 115 120 125	680
GTG GGC TGC TTC CTC TTT GGC TGT GCC ATC AGC CAG TCT TTC ACA GAC Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr Asp 130 135 140 145	728
ATT GCC AAA GTG TCC ATA GGG CGC CTG CGT CCT CAC TTC TTG AGT GTC Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser Val 150 155 160	776
TGC AAC CCT GAT TTC AGC CAG ATC AAC TGC TCT GAA GGC TAC ATT CAG Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile Gln 165 170 175	824
AAC TAC AGA TGC AGA GGT GAT GAC AGC AAA GTC CAG GAA GCC AGG AAG Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg Lys 180 185 190	872
TCC TTC TTC TCT GGC CAT GCC TCC TTC TCC ATG TAC ACT ATG CTG TAT Ser Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu Tyr 195 200 205	920
TTG GTG CTA TAC CTG CAG GCC CGC TTC ACT TGG CGA GGA GCC CGC CTG Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg Leu 210 215 220 225	968
CTC CGG CCC CTC CTG CAG TTC ACC TTG ATC ATG ATG GCC TTC TAC ACG Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr Thr 230 235 240	1016
GGA CTG TCT CGC GTA TCA GAC CAC AAG CAC CAT CCC AGT GAT GTT CTG Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val Leu 245 250 255	1064
GCA GGA TTT GCT CAA GGA GCC CTG GTG GCC TGC ATA GTT TTC TTC Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe Phe 260 265 270	1112
GTG TCT GAC CTC TTC AAG ACT AAG ACG ACG CTC TCC CTG CCT GCC CCT Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala Pro 275 280 285	1160
GCT ATC CGG AAG GAA ATC CTT TCA CCT GTG GAC ATT ATT GAC AGG AAC Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg Asn 290 295 300 305	1208
AAT CAC CAC AAC ATG ATG TAGGTGCCAC CCACCTCCTG AGCTGTTTTT Asn His His Asn Met Met 310	1256
GTAAAATGAC TGCTGACAGC AAGTTCTTGC TGCTCTCAA TCTCATCAGA CAGTAGAATG	1316
TAGGGAAAAA CTTTGCCCCG ACTGATTTT AAAAAAAA AAAAAA	1362

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 311 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn  
1 5 10 15

Gly Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys  
20 25 30

Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly  
35 40 45

Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg  
50 55 60

Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly  
65 70 75 80

Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala  
85 90 95

Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys  
100 105 110

Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys  
115 120 125

Gln Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr  
130 135 140

Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser  
145 150 155 160

Val Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile  
165 170 175

Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg  
180 185 190

Lys Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu  
195 200 205

Tyr Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg  
210 215 220

Leu Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr  
225 230 235 240

Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val  
245 250 255

Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe  
260 265 270

Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Leu Ser Leu Pro Ala  
275 280 285

Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg  
290 295 300

Asn Asn His His Asn Met Met  
305 310

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 4..833

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 4..833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACC ATG CAG CGG AGG TGG GTC TTC GTG CTG CTC GAC GTC CTG TGC TTA	48
Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu	
1 5 10 15	
CTG GTC GCC TCC CTG CCC TTC GCT ATC CTG ACG CTG GTG AAC GCC CCG	96
Leu Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro	
20 25 30	
TAC AAG CGA GGA TTT TAC TGC GGG GAT GAC TCC ATC CGG TAC CCC TAC	144
Tyr Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr	
35 40 45	
CGT CCA GAT ACC ATC ACC CAC GGG CTC ATG GCT GGG GTC ACC ATC ACG	192
Arg Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr	
50 55 60	
GCC ACC GTC ATC CTT GTC TCG GCC GGG GAA GCC TAC CTG GTG TAC ACA	240
Ala Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr	
65 70 75	
GAC CGG CTC TAT TCT CGC TCG GAC TTC AAC AAC TAC GTG GCT GCT GTA	288
Asp Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val	
80 85 90 95	
TAC AAG GTG CTG GGG ACC TTC CTG TTT GGG GCT GCC GTG AGC CAG TCT	336
Tyr Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser	
100 105 110	
CTG ACA GAC CTG GCC AAG TAC ATG ATT GGG CGT CTG AAG CCC AAC TTC	384
Leu Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe	
115 120 125	
CTA GCC GTC TGC GAC CCC GAC TGG AGC CGG GTC AAC TGC TCG GTC TAT	432
Leu Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr	
130 135 140	
GTG CAG CTG GAG AAG GTG TGC AGG GGA AAC CCT GCT GAT GTC ACC GAG	480
Val Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu	
145 150 155	
GCC AGG TTG TCT TTC TAC TCG GGA CAC TCT TCC TTT GGG ATG TAC TGC	528
Ala Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys	
160 165 170 175	

ATG GTG TTC TTG GCG CTG TAT GTG CAG GCA CGA CTC TGT TGG AAG TGG Met Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp	576
180 185 190	
GCA CGG CTG CTG CGA CCC ACA GTC CAG TTC TTC CTG GTG GCC TTT GCC Ala Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala	624
195 200 205	
CTC TAC GTG GGC TAC ACC CGC GTG TCT GAT TAC AAA CAC CAC TGG AGC Leu Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser	672
210 215 220	
GAT GTC CTT GTT GGC CTC CTG CAG GGG GCA CTG GTG GCT GCC CTC ACT Asp Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr	720
225 230 235	
GTC TGC TAC ATC TCA GAC TTC TTC AAA GCC CGA CCC CCA CAG CAC TGT Val Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys	768
240 245 250 255	
CTG AAG GAG GAG GAG CTG GAA CGG AAG CCC AGC CTG TCA CTG ACG TTG Leu Lys Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu	816
260 265 270	
ACC CTG GGG CGA GGC TG ACCACAACCA CTTATGGGAT ACCCGCACTC Thr Leu Gly Arg Gly	863
275	
TTCTTCCTGA GGCGGGACCC CGCCCAGGCA GGGAGCTGCT GTGAGTCCAG CTGATGCCCA	923
CCCAGGGTGGT CCCTCCAGCC TGGTAGGC A CTGAGGGTTC TGGACGGGCT CCAGGAACCC	983
TGGGCTGATG GGAGCAGTGA GCGGTTCCGC TGCCCCCTGC CCTGCACTGG ACCAGGAGTC	1043
TGGAGATGCC TGGGTAGCCC TCAGCATTTG GAGGGGAACC TGTTCGGTC GGTCCCCAAA	1103
TATCCCCCTTC TTTTTATGGG GTTAAGGAAG GGACCGAGAG ATCAGATAGT TGCTGTTTG	1163
TAAAATGTAA TGTATATGTG GTTTTTAGTA AAATAGGGCA CCTGTTTCAC AAAAAAAA	1223
AAAAAAA	1232

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 276 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gln Arg Arg Trp Val Phe Val Leu Asp Val Leu Cys Leu Leu	
1 5 10 15	
Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro Tyr	
20 25 30	
Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr Arg	
35 40 45	
Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr Ala	
50 55 60	

Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp  
65 70 75 80

Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr  
85 90 95

Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu  
100 105 110

Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu  
115 120 125

Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val  
130 135 140

Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala  
145 150 155 160

Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met  
165 170 175

Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala  
180 185 190

Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu  
195 200 205

Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp  
210 215 220

Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val  
225 230 235 240

Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu  
245 250 255

Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr  
260 265 270

Leu Gly Arg Gly  
275

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Ile Cys  
1 5 10 15

Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr  
20 25 30

Pro Phe Gln Arg Gly Ile Phe Cys Asn Asp Asp Ser Ile Lys Tyr Pro  
35 40 45

Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Val Ile  
50 55 60

Pro Phe Cys Ile Ile Val Met Ser Ile Gly Glu Ser Leu Ser Val Tyr  
65 70 75 80

Phe Asn Val Leu His Ser Asn Ser Phe Val Gly Asn Pro Tyr Ile Ala  
85 90 95

Thr Ile Tyr Lys Ala Val Gly Ala Phe Leu Phe Gly Val Ser Ala Ser  
100 105 110

Gln Ser Leu Thr Asp Ile Ala Lys Tyr Thr Ile Gly Ser Leu Arg Pro  
115 120 125

His Phe Leu Ala Ile Cys Asn Pro Asp Trp Ser Lys Ile Asn Cys Ser  
130 135 140

Asp Gly Tyr Ile Glu Asp Tyr Ile Cys Gln Gly Asn Glu Glu Lys Val  
145 150 155 160

Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met  
165 170 175

Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly  
180 185 190

Asp Trp Ala Arg Leu Leu Arg Pro Met Leu Gln Phe Gly Leu Ile Ala  
195 200 205

Phe Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His  
210 215 220

Trp Ser Asp Val Thr Val Gly Leu Ile Gln Gly Ala Ala Met Ala Ile  
225 230 235 240

Leu Val Ala Leu Tyr Val Ser Asp Phe Phe Lys Asp Thr His Ser Tyr  
245 250 255

Lys Glu Arg Lys Glu Glu Asp Pro His Thr Thr Leu His Glu Thr Ala  
260 265 270

Ser Ser Arg Asn Tyr Ser Thr Asn His Glu Pro  
275 280

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys  
1 5 10 15

Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr  
20 25 30

Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro  
35 40 45

Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile  
50 55 60

Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr  
65 70 75 80

Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala  
85 90 95

Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser  
100 105 110

Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro  
115 120 125

His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser  
130 135 140

Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val  
145 150 155 160

Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met  
165 170 175

Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly  
180 185 190

Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala  
195 200 205

Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His  
210 215 220

Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile  
225 230 235 240

Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe  
245 250 255

Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro  
260 265 270

Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
275 280

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys  
1 5 10 15

Val Leu Leu Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile  
20 25 30

Tyr Pro Phe Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr  
35 40 45

Pro Tyr His Asp Ser Thr Ala Ala Ser Thr Val Leu Ile Leu Val Gly  
50 55 60

Val Gly Leu Pro Val Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val  
65 70 75 80

Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile  
85 90 95

Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala  
100 105 110

Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg  
115 120 125

Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys  
130 135 140

Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg  
145 150 155 160

Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser  
165 170 175

Met Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys  
180 185 190

Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val  
195 200 205

Ala Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His  
210 215 220

His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala  
225 230 235 240

Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser  
245 250 255

Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr  
260 265 270

Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
275 280 285

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn  
1 5 10 15

Gly Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys  
20 25 30

Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly  
35 40 45

Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg  
50 55 60

Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly  
65 70 75 80

Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala  
85 90 95

Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys  
100 105 110

Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys  
115 120 125

Gln Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr  
130 135 140

Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser  
145 150 155 160

Val Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile  
165 170 175

Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg  
180 185 190

Lys Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu  
195 200 205

Tyr Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg  
210 215 220

Leu Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr  
225 230 235 240

Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val  
245 250 255

Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe  
260 265 270

Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala  
275 280 285

Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg  
290 295 300

Asn Asn His His Asn Met Met  
305 310

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu Leu  
1 5 10 15

Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro Tyr  
20 25 30

Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr Arg  
35 40 45

Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr Ala  
50 55 60

Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp  
65 70 75 80

Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr  
85 90 95

Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu  
100 105 110

Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu  
115 120 125

Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val  
130 135 140

Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala  
145 150 155 160

Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met  
165 170 175

Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala  
180 185 190

Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu  
195 200 205

Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp  
210 215 220

Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val  
225 230 235 240

Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu  
245 250 255

Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr  
260 265 270

Leu Gly Arg Gly  
275

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCTCTAGAT ATTAATAGTA ATCAATTAC

29

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCACGCAT GCACCATGGT AATAGC

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(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTGCATGCG TGAGGCTCCG GTGC

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAGTTTCA CGGTACCTGA AATGGAAG

28

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCATGGTAC CATGTTTGAC AAGACGCGGC

30

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CATATGAGT ATTCAATGTA ACC

23

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGATGGCTAG CATGCAGAGA AGATGGGTCT TCGTGCTGCT CGACGTG

47

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGTGCGGGAT CCCATAAGTG GTTG

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 077319/0125

In re patent application of

David W. LEUNG *et al.*

Serial No. 08/842,827

Group Art Unit: 1801

Filed: April 17, 1997

Examiner: Unassigned

For: HUMAN PHOSPHATIDIC ACID PHOSPHATASE

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents  
Washington, D.C. 20231  
Box SEQUENCE

Sir:

In response to the Notice to Comply With Requirements for Applications Containing Sequence Disclosures mailed June 9, 1997, please amend the application as follows:

IN THE SPECIFICATION:

Page 3, line 22, after "284" insert --(SEQ ID NO:2)--;  
line 24, after "285" insert --(SEQ ID NO:4)--;  
line 25, after "276" insert --(SEQ ID NO:8)--;  
line 30, after "284" insert --(SEQ ID NO:2)--;  
line 31, after "285" insert --(SEQ ID NO:4)--;  
line 33, after "276" insert --(SEQ ID NO:8)--.

Page 4, line 23, after "sequence" insert --(SEQ ID  
NOS:1 and 2)--;  
line 26, after "sequence" insert --(SEQ ID  
NOS:3 and 4)--;  
line 29, after "sequence" insert --(SEQ ID  
NOS:5 and 6)--;  
line 32, after "sequence" insert --(SEQ ID  
NOS:7 and 8)--;

line 33, after "sequences" insert --(SEQ ID NOS:9-13)---.

Page 7, line 35, after "4" insert --(SEQ ID NOS:2, 4, 6 and 8)---.

Page 10, line 18, after "1193" insert --of SEQ ID NO:1---;

line 19, after "1196" insert --of SEQ ID NO:3---; delete "amino acid number";

line 20, delete "1 to amino acid number 311" and insert --nucleotide number 294 to nucleotide number 1226 of SEQ ID NO:5---;

line 21, after "833" insert --of SEQ ID NO:7---.

Page 11, line 12, after "4" insert --(SEQ ID NOS:1, 3, 5 and 7)---.

Page 14, line 31, after "3'" insert --(SEQ ID NO:14)---;

line 32, after "3'" insert --(SEQ ID NO:15)---;

line 36, after "3'" insert --(SEQ ID NO:16)---.

Page 15, line 1, after "3'" insert --(SEQ ID NO:17)---.

Page 18, line 34, after "3'" insert --(SEQ ID NO:18)---;

line 35, after "3'" insert --(SEQ ID NO:19)---.

Page 19, line 25, after "3'" insert --(SEQ ID NO:14)---;

line 26, after "3'" insert --(SEQ ID NO:15)---;

line 30, after "3'" insert --(SEQ ID NO:16)---;

line 31, after "3'" insert --(SEQ ID NO:17)---.

Page 20, line 4, after "3'" insert --(SEQ ID NO:20)---;

line 6, after "3'" insert --(SEQ ID NO:21)---;

line 15, before "respectively" insert --(SEQ ID NOS:1, 3, 5 and 7)--;

line 21, after "4" insert --, SEQ ID NOS:2, 4, 6 and 8--.

Page 22, at the end of the specification, before the claims, insert the printed Sequence Listing submitted concurrently herewith, and renumber pages 1-19 of the Sequence Listing as pages 23-41 of the specification.

IN THE CLAIMS:

Please renumber pages 23-24 as pages 42-43 and amend the claims as follows.

1. (Amended) An isolated polynucleotide encoding human phosphatidic acid phosphatase wherein said polynucleotide encodes a protein comprising a polypeptide sequence selected from the group consisting of (i) the sequence at amino acid number 1 to amino acid number 284 in Figure 1 (SEQ ID NO:2), (ii) the sequence at amino acid number 1 to amino acid number 285 in Figure 2 (SEQ ID NO:4), and (iii) the sequence at amino acid number 1 to amino acid number 276 in Figure 4 (SEQ ID NO:8).

2. (Amended) An isolated human phosphatidic acid phosphatase protein, wherein said protein comprises a polypeptide sequence selected from the group consisting of (i) the sequence at amino acid number 1 to amino acid number 284 in Figure 1 (SEQ ID NO:2), (ii) the sequence at amino acid number 1 to amino acid number 285 in Figure 2 (SEQ ID NO:4), and (iii) the sequence at amino acid number 1 to amino acid number 276 in Figure 4 (SEQ ID NO:8).

4. (Amended) The method of claim 3, wherein said polynucleotide encoding human phosphatidic acid is selected from the group consisting of (i) the sequence at amino acid number 1 to amino acid number 284 in Figure 1 (SEQ ID NO:2), (ii) the sequence at amino acid number 1 to amino acid number 285 in Figure 2 (SEQ ID NO:4), (iii) the sequence at amino acid number 1 to amino acid number 311 in Figure 3 (SEQ ID NO:6), and (iv) the sequence at amino acid number 1 to amino acid number 276 in Figure 4 (SEQ ID NO:8).

Claim 6, line 3, after "1" insert --(SEQ ID NO:2)---.

Claim 7, line 3, after "2" insert --(SEQ ID NO:4)---.

Claim 8, line 3, after "3" insert --(SEQ ID NO:6)---.

Claim 9, line 3, after "4" insert --(SEQ ID NO:8)---.

REMARKS

Applicants submit this Preliminary Amendment to insert required references to SEQ ID NOS of the Sequence Listing filed concurrently herewith, to indicate the insertion point for the Sequence Listing, and to effect the necessary changes in pagination. Applicants also have corrected a typographical error appearing at page 10, lines 19-20. Applicants respectfully request examination on the merits of this application.

It is believed that no additional fees are required; however, the Commissioner is hereby authorized to charge any deficiency or credit any overpayment to Deposit Account No. 19-0741. It is further believed that no additional petition for an extension of time under 37 C.F.R. § 1.136 is required. However, should such a petition be required, applicant hereby petitions the Commissioner for an extension of time, and authorizes the Commissioner to charge the necessary petition fee to Deposit Account No. 19-0741.

Respectfully submitted,

5 August 1987  
Date

S. A. Bent  
Stephen A. Bent  
Reg. No. 29,768

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AUG  
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1997MAIL ROOM  
DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address, and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**HUMAN PHOSPHATIDIC ACID PHOSPHATASE**

the specification of which is attached hereto unless the following box is checked:

 was filed on April 17, 1997 as United States Application Number or PCT International Application Number 08/842,827  
and was amended on \_\_\_\_\_ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is known by me to be material to patentability as defined in Title 37, Code of Federal Regulations § 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 363(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed:

**PRIOR FOREIGN APPLICATION(S)**

NUMBER	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED

I hereby claim the benefit under Title 35, United States Code § 119(e) of any United States provisional application(s) listed below.

APPLICATION NO.	FILING DATE

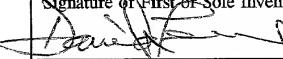
I hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s), or § 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I acknowledge the duty to disclose information which is known by me to be material to patentability as defined in Title 37, Code of Federal Regulations § 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

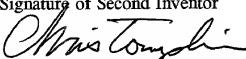
APPLICATION SERIAL NO.	FILING DATE	STATUS: PATENTED, PENDING, ABANDONED

I hereby appoint as my attorneys, with full powers of substitution and revocation, to prosecute this application and transact all business in the Patent and Trademark Office connected therewith: Stephen A. Bent, Reg. No. 29,768; David A. Blumenthal, Reg. No. 26,257; William T. Ellis, Reg. No. 26,874; John J. Feldhaus, Reg. No. 28,822; Patricia D. Granados, Reg. No. 33,683; John P. Isaacson, Reg. No. 33,715; Donald D. Jeffery, Reg. No. 19,980; Eugene M. Lee, Reg. No. 32,039; Peter G. Mack, Reg. No. 26,001; Brian J. McNamara, Reg. No. 32,789; Sybil Melloy, Reg. No. 22,749; George E. Quillin, Reg. No. 32,792; Colin G. Sandercock, Reg. No. 31,298; Bernhard D. Saxe, Reg. No. 28,663; Charles F. Schill, Reg. No. 27,590; Richard L. Schwab, Reg. No. 25,479; Arthur Schwartz, Reg. No. 22,115; Harold C. Wegner, Reg. No. 25,258.

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Address telephone communications to John P. Isaacson at (202) 672-5300.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of First or Sole Inventor <u>David W. LEUNG</u> 1-00	Signature of First or Sole Inventor 	Date 7/16/997
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Post Office Address <u>7625 E. Mercer Way, Mercer Island, Washington 98040</u>		

Full Name of Second Inventor <u>Christopher K. TOMPKINS</u> 2-00	Signature of Second Inventor 	Date 7/16/997
Residence Address <u>Bothell, Washington</u> WA	Country of Citizenship USA	
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Applicant or Patentee: David W. LEUNG et al  
Serial or Patent No.: 08/842,827 Atty. Dkt. No. 077319/0125  
Filed or Issued: April 17, 1997  
FOR HUMAN PHOSPHATIDYL ACID PHOSPHATASE

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS  
(37 CFR 1.9(f) AND 1.27 (c)) – SMALL BUSINESS CONCERN**

I declare that I am  
( ) the owner of the small business concern identified below:  
( ) an official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN CELL THERAPEUTICS, INC.  
ADDRESS OF CONCERN Suite #401, 201 Elliott Avenue, West, Seattle, Washington, 98119

I hereby declare that the above-identified small business concern qualifies as a small business concern as defined in 13 CFR 121.3-18 and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled HUMAN PHOSPHATIDIC ACID PHOSPHATASE by inventor(s) David W. LEUNG et al., described in

( ) the specification filed herewith  
(x) application serial no. 08/842,827, filed April 17, 1997  
( ) patent no.   , issued

If the rights held by the above-identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below\* and no rights to the invention are held by any person, other than the inventor, who would not qualify as an independent inventor under 37 CFR 1.9(c) if that person made the invention, or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e). \* NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities: (37 CFR 1.27)

NAME: \_\_\_\_\_  
ADDRESS: \_\_\_\_\_  
 INDIVIDUAL       SMALL BUSINESS CONCERN       NONPROFIT CORPORATION

NAME: \_\_\_\_\_  
ADDRESS: \_\_\_\_\_  
() INDIVIDUAL      () SMALL BUSINESS CONCERN      () NONPROFIT CORPORATION

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate: (37 CFR 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING: Maurice J. Schwarz, PhD  
TITLE OF PERSON OTHER THAN OWNER: EVP, Product Development  
ADDRESS OF PERSON SIGNING: 201 Elliott Avenue West, Suite 400, Seattle, WA 98119  
SIGNATURE:  DATE: 7/16/17